

SEQUENCE LISTING

70880

<110> SHEPPARD, PAUL O.
JASPERS, STEPHEN R.
DEISHER, THERESA A.
BISHOP, PAUL D.

<120> METHOD OF FORMING A PEPTIDE-RECEPTOR
COMPLEX WITH ZSIG33

<130> 99-62

<150> 60/166,765

<151> 1999-11-22

<160> 16

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(351)

<400> 1

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Met	Pro	Ser	Pro	Gly	Thr	Val	Cys	Ser	Leu	Leu	Leu	Leu	Gly	Met	Leu	
1				5					10					15		

tgg	ctg	gac	ttg	gcc	atg	gca	ggc	tcc	agc	ttc	ctg	agc	cct	gaa	cac	96
Trp	Leu	Asp	Leu	Ala	Met	Ala	Gly	Ser	Ser	Phe	Leu	Ser	Pro	Glu	His	
		20					25						30			

cag	aga	gtc	cag	cag	aga	aag	gag	tcg	aag	aag	cca	cca	gcc	aag	ctg	144
Gln	Arg	Val	Gln	Gln	Arg	Lys	Glu	Ser	Lys	Lys	Pro	Pro	Ala	Lys	Leu	
		35					40					45				

cag ccc cga gct cta gca ggc tgg ctc cgc ccg gaa gat gga ggt caa 192
 Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln
 50 55 60

gca gaa ggg gca gag gat gaa ctg gaa gtc cgg ttc aac gcc ccc ttt 240
 Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe
 65 70 75 80

gat gtt gga atc aag ctg tca ggg gtt cag tac cag cag cac agc cag 288
 Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln
 85 90 95

gcc ctg ggg aag ttt ctt cag gac atc ctc tgg gaa gag gcc aaa gag 336
 Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu
 100 105 110

gcc cca gcc gac aag 351
 Ala Pro Ala Asp Lys
 115

<210> 2

<211> 117

<212> PRT

<213> Homo sapiens

<400> 2

Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Gly Met Leu
 1 5 10 15
 Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His
 20 25 30
 Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu
 35 40 45
 Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln
 50 55 60
 Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe
 65 70 75 80
 Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln
 85 90 95
 Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu
 100 105 110

115

<211> 351

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Degenerate polynucleotide

<221> misc feature

 $\langle 222 \rangle \quad (1) \dots (351)$

<223> n = A, T, C or G

<400> 3

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gcnatggcng	gnwsnwsntt	yytnwsnccn	garcaycarm	nggtncarca	rmgnaargar	120
wsnaaaraarc	cncncgcnaa	rytncarccn	mgngcnytn	cnggntggyt	nmgnccngar	180
gayggnggnc	argcngargg	ngcngargay	garytnarg	tnmgnttyaa	ygcnccntty	240
gaygtnggna	thaarytnws	nggngtncar	taycarcarc	aywsncargc	nytnggnaar	300
ttyytncarg	ayathytn	tgargargcn	aargargcnc	cngcngayaa	r	351

<210> 4

$\langle 211 \rangle$ 1101

<212> DNA

<213> Homo sapiens

$\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1101)$

<400> 4

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Met Trp Asn Ala Thr Pro Ser Glu Glu Pro Gly Phe Asn Leu Thr Leu
1 5 10 15

gcc gac ctg gac tgg gat gct tcc ccc ggc aac gac tcg ctg ggc gac 96
Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp
20 25 30

gag ctg ctg cag ctc ttc ccc gcg ccg ctg ctg gcg ggc gtc aca gcc Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala 35 40 45	144
acc tgc gtg gca ctc ttc gtg gtg ggt atc gct ggc aac ctg ctc acc Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr 50 55 60	192
atg ctg gtg gtg tcg cgc ttc cgc gag ctg cgc acc acc acc aac ctc Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu 65 70 75 80	240
tac ctg tcc agc atg gcc ttc tcc gat ctg ctc atc ttc ctc tgc atg Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met 85 90 95	288
ccc ctg gac ctc gtt cgc ctc tgg cag tac cgg ccc tgg aac ttc ggc Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly 100 105 110	336
gac ctc ctc tgc aaa ctc ttc caa ttc gtc agt gag agc tgc acc tac Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr 115 120 125	384
gcc acg gtg ctc acc atc aca gcg ctg agc gtc gag cgc tac ttc gcc Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala 130 135 140	432
atc tgc ttc cca ctc cgg gcc aag gtg gtg gtc acc aag ggg cgg gtg Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val 145 150 155 160	480
aag ctg gtc atc ttc gtc atc tgg gcc gtg gcc ttc tgc agc gcc ggg Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly 165 170 175	528
ccc atc ttc gtg cta gtc ggg gtg gag cac gag aac ggc acc gac cct Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro 180 185 190	576

tgg gac acc aac gag tgc cgc ccc acc gag ttt gcg gtg cgc tct gga Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly 195 200 205	624
ctg ctc acg gtc atg gtg tgg gtg tcc agc atc ttc ttc ttc ctt cct Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro 210 215 220	672
gtc ttc tgt ctc acg gtc ctc tac agt ctc atc ggc agg aag ctg tgg Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp 225 230 235 240	720
cgg agg agg cgc ggc gat gct gtc gtg ggt gcc tcg ctc agg gac cag Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln 245 250 255	768
aac cac aag caa acc gtg aaa atg ctg gct gta gtg gtg ttt gcc ttc Asn His Lys Gln Thr Val Lys Met Leu Ala Val Val Val Phe Ala Phe 260 265 270	816
atc ctc tgc tgg ctc ccc ttc cac gta ggg cga tat tta ttt tcc aaa Ile Leu Cys Trp Leu Pro Phe His Val Gly Arg Tyr Leu Phe Ser Lys 275 280 285	864
tcc ttt gag cct ggc tcc ttg gag att gct cag atc agc cag tac tgc Ser Phe Glu Pro Gly Ser Leu Glu Ile Ala Gln Ile Ser Gln Tyr Cys 290 295 300	912
aac ctc gtg tcc ttt gtc ctc ttc tac ctc agt gct gcc atc aac ccc Asn Leu Val Ser Phe Val Leu Phe Tyr Leu Ser Ala Ala Ile Asn Pro 305 310 315 320	960
att ctg tac aac atc atg tcc aag aag tac cgg gtg gca gtg ttc aga Ile Leu Tyr Asn Ile Met Ser Lys Lys Tyr Arg Val Ala Val Phe Arg 325 330 335	1008
ctt ctg gga ttc gaa ccc ttc tcc cag aga aag ctc tcc act ctg aaa Leu Leu Gly Phe Glu Pro Phe Ser Gln Arg Lys Leu Ser Thr Leu Lys 340 345 350	1056

gat gaa agt tct cgg gcc tgg aca gaa tct agt att aat aca tga 1101
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 355 360 365

<210> 5
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 5
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 1 5 10 15
 Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp
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 Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala
 35 40 45
 Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr
 50 55 60
 Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu
 65 70 75 80
 Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met
 85 90 95
 Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly
 100 105 110
 Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr
 115 120 125
 Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
 130 135 140
 Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
 145 150 155 160
 Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly
 165 170 175
 Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro
 180 185 190
 Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly
 195 200 205
 Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro
 210 215 220
 Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp
 225 230 235 240

Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln
 245 250 255
 Asn His Lys Gln Thr Val Lys Met Leu Ala Val Val Val Phe Ala Phe
 260 265 270
 Ile Leu Cys Trp Leu Pro Phe His Val Gly Arg Tyr Leu Phe Ser Lys
 275 280 285
 Ser Phe Glu Pro Gly Ser Leu Glu Ile Ala Gln Ile Ser Gln Tyr Cys
 290 295 300
 Asn Leu Val Ser Phe Val Leu Phe Tyr Leu Ser Ala Ala Ile Asn Pro
 305 310 315 320
 Ile Leu Tyr Asn Ile Met Ser Lys Lys Tyr Arg Val Ala Val Phe Arg
 325 330 335
 Leu Leu Gly Phe Glu Pro Phe Ser Gln Arg Lys Leu Ser Thr Leu Lys
 340 345 350
 Asp Glu Ser Ser Arg Ala Trp Thr Glu Ser Ser Ile Asn Thr
 355 360 365

<210> 6
 <211> 1098
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate sequence

<221> misc_feature
 <222> (1)...(1098)
 <223> n = A,T,C or G

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 tgggaygcnw snccnggnaa ygaywsnytn ggngaygary tnytnaryt nttyccngcn 120
 ccnytnytng cngngtnac ngcnactgy gtngcnytn tygtngtnng nathgcnggn 180
 aayytntytna cnatgytngt ngtnwsnmgn ttymngary tnmgnacnac nacnaayytn 240
 taytnwsnw snatggcntt ywsngayytn ytnathttyy tntgyatgcc nytngayytn 300
 gtnmgnytn tggcartaymg nccntggaay ttyggngayy tnytnntyaa rytnnttycar 360
 ttygtwnsng arwsntgyac ntaygcnacn gtynytnacna thacngcny twnsngtngar 420
 mgntayttyg cnathtgytt yccnytnmgn gcnargtn tngtnacnaa rggnmngtn 480
 aarytngtna thttgytnat htggcngtn gcnttytygw sngcnggncc nathttygtn 540
 ytngtngng tngarcayga raaygnacn gayccntggg ayacnaayga rtgymngccn 600

acngarttyg	cngtnmgmws	nggnytnytn	acngtnatgg	tntgggtnws	nwsnathtty	660
ttyttytnc	cngtnttytg	yytnacngtn	ytntaywsny	tnathggnmg	naarytntgg	720
mgnmgmgnm	gngngaygc	ngtngtnggn	gcnwsnytnm	gngaycaraa	ycayaarcac	780
acngtnaara	tgytngcngt	ngtngtntty	gcnttyathy	tntgytggyt	nccnttycay	840
gtnggnmgnt	ayytnttyws	naarwsntty	garccnggnw	snytnngarat	hgcnarath	900
wsncartayt	gyaaytngt	nwsnttygtn	ytnttytayy	tnwsngcngc	nathaayccn	960
athytntaya	ayathatgws	naaraartay	mgngtngcng	tntymgnyt	nytnggntty	1020
garccnttyw	sncarmgnaa	rytnwsnacd	ytnaargayg	arwsnwsnmg	ngcntggacn	1080
garwsnwsna	thaayacn					1098

<210> 7

<211> 546

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (40)...(396)

<400> 7

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gct	gtg	gtc	gtc	ctg	ctg	gtg	gtg	cac	gca	gct	gcc	atg	ctg	gcc	tcc	102
Ala	Val	Val	Val	Leu	Leu	Val	Val	His	Ala	Ala	Ala	Met	Leu	Ala	Ser	
				10				15						20		

cac	acg	gaa	gcc	ttt	gtt	ccc	agc	ttt	acc	tac	ggg	gaa	ctt	cag	agg	150
His	Thr	Glu	Ala	Phe	Val	Pro	Ser	Phe	Thr	Tyr	Gly	Glu	Leu	Gln	Arg	
		25					30						35			

atg	cag	gaa	aag	gag	cgg	aat	aaa	ggg	caa	aag	aaa	tcc	ctg	agt	gtc	198
Met	Gln	Glu	Lys	Glu	Arg	Asn	Lys	Gly	Gln	Lys	Lys	Ser	Leu	Ser	Val	
	40					45						50				

cag	cag	gcg	tcg	gag	gag	ctc	ggc	cct	ctg	gac	ccc	tcg	gag	ccc	acg	246
Gln	Gln	Ala	Ser	Glu	Glu	Leu	Gly	Pro	Leu	Asp	Pro	Ser	Glu	Pro	Thr	
	55					60					65					

aag gaa gaa gaa agg gtg gtt atc aag ctg ctc gcg cct gtg gac att 294
 Lys Glu Glu Glu Arg Val Val Ile Lys Leu Leu Ala Pro Val Asp Ile
 70 75 80 85

gga atc agg atg gac tcc agg cag ctg gaa aag tac cgg gcc acc ctg 342
 Gly Ile Arg Met Asp Ser Arg Gln Leu Glu Lys Tyr Arg Ala Thr Leu
 90 95 100

gaa agg ctg ctg ggc cag gcg ccg cag tcc acc cag aac cag aat gcc 390
 Glu Arg Leu Leu Gly Gln Ala Pro Gln Ser Thr Gln Asn Gln Asn Ala
 105 110 115

gcc aag taacaggccg ctgggggaga aggaggacac agctcggacc cccctccac 446
 Ala Lys

gcagggaggg cctagaaatc cgctgggctt ggaaggaaaa caccctctcc caaacagccc 506
 tcagcccccc tccccagca aataaagcgt ggaaataggc 546

<210> 8

<211> 119

<212> PRT

<213> Sus scrofa

<400> 8

Met Val Ser Arg Lys Ala Val Val Val Leu Leu Val Val His Ala Ala
 1 5 10 15
 Ala Met Leu Ala Ser His Thr Glu Ala Phe Val Pro Ser Phe Thr Tyr
 20 25 30
 Gly Glu Leu Gln Arg Met Gln Glu Lys Glu Arg Asn Lys Gly Gln Lys
 35 40 45
 Lys Ser Leu Ser Val Gln Gln Ala Ser Glu Glu Leu Gly Pro Leu Asp
 50 55 60
 Pro Ser Glu Pro Thr Lys Glu Glu Glu Arg Val Val Ile Lys Leu Leu
 65 70 75 80
 Ala Pro Val Asp Ile Gly Ile Arg Met Asp Ser Arg Gln Leu Glu Lys
 85 90 95
 Tyr Arg Ala Thr Leu Glu Arg Leu Leu Gly Gln Ala Pro Gln Ser Thr
 100 105 110
 Gln Asn Gln Asn Ala Ala Lys
 115

<210> 9
 <211> 1239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1239)

<400> 9

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Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu	
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ccg ccg tgg ccc gcg ctg ccg cct tgc gac gag cgc cgc tgc tcg ccc	96
Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro	
20 25 30	
ttt ccc ctg ggg gcg ctg gtg ccg gtg acc gct gtg tgc ctg tgc ctg	144
Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu	
35 40 45	
ttc gtc gtc ggg gtg agc ggc aac gtg gtg acc gtg atg ctg atc ggg	192
Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly	
50 55 60	
cgc tac cgg gac atg cgg acc acc acc aac ttg tac ctg ggc agc atg	240
Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met	
65 70 75 80	
gcc gtg tcc gac cta ctc atc ctg ctc ggg ctg ccg ttc gac ctg tac	288
Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr	
85 90 95	
cgc ctc tgg cgc tcg cgg ccc tgg gtg ttc ggg ccg ctg ctc tgc cgc	336
Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg	
100 105 110	

ctg tcc ctc tac gtg ggc gag ggc tgc acc tac gcc acg ctg ctg cac	384
Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His	
115 120 125	
atg acc gcg ctc agc gtc gag cgc tac ctg gcc atc tgc cgc ccg ctc	432
Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu	
130 135 140	
cgc gcc cgc gtc ttg gtc acc cgg cgc cgc gtc cgc gcg ctc atc gct	480
Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala	
145 150 155 160	
gtg ctc tgg gcc gtg gcg ctg ctc tct gcc ggt ccc ttc ttg ttc ctg	528
Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu	
165 170 175	
gtg ggc gtc gag cag gac ccc ggc atc tcc gta gtc ccg ggc ctc aat	576
Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn	
180 185 190	
ggc acc gcg cgg atc gcc tcc tcg cct ctc gcc tcg tcg ccg cct ctc	624
Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu	
195 200 205	
tgg ctc tcg cgg gcg cca ccg ccg tcc ccg ccg tcg ggg ccc gag acc	672
Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr	
210 215 220	
gcg gag gcc gcg gcg ctg ttc agc cgc gaa tgc cgg ccg agc ccc gcg	720
Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala	
225 230 235 240	
cag ctg ggc gcg ctg cgt gtc atg ctg tgg gtc acc acc gcc tac ttc	768
Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe	
245 250 255	
ttc ctg ccc ttt ctg tgc ctc agc atc ctc tac ggg ctc atc ggg cgg	816
Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg	
260 265 270	

gag ctg tgg agc agc cgg cgg ccg ctg cga ggc ccg gcc gcc tcg ggg Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly 275 280 285	864
cgg gag aga ggc cac cgg cag acc gtc cgc gtc ctg ctg gtg gtg gtt Arg Glu Arg Gly His Arg Gln Thr Val Arg Val Leu Leu Val Val Val 290 295 300	912
ctg gca ttt ata att tgc tgg ttg ccc ttc cac gtt ggc aga atc att Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile 305 310 315 320	960
tac ata aac acg gaa gat tcg cgg atg atg tac ttc tct cag tac ttt Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe 325 330 335	1008
aac atc gtc gct ctg caa ctt ttc tat ctg agc gca tct atc aac cca Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro 340 345 350	1056
atc ctc tac aac ctc att tca aag aag tac aga gcg gcg gcc ttt aaa Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Ala Phe Lys 355 360 365	1104
ctg ctg ctc gca agg aag tcc agg ccg aga ggc ttc cac aga agc agg Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg 370 375 380	1152
gac act gcg ggg gaa gtt gca ggg gac act gga gga gac acg gtg ggc Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly 385 390 395 400	1200
tac acc gag aca agc gct aac gtg aag acg atg gga taa Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly *	1239
405 410	

<210> 10

<211> 412

<212> PRT

<213> Homo sapiens

<400> 10

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Pro	Pro	Trp	Pro	Ala	Leu	Pro	Pro	Cys	Asp	Glu	Arg	Arg	Cys	Ser	Pro
			20					25					30		
Phe	Pro	Leu	Gly	Ala	Leu	Val	Pro	Val	Thr	Ala	Val	Cys	Leu	Cys	Leu
		35					40					45			
Phe	Val	Val	Gly	Val	Ser	Gly	Asn	Val	Val	Thr	Val	Met	Leu	Ile	Gly
	50					55					60				
Arg	Tyr	Arg	Asp	Met	Arg	Thr	Thr	Thr	Asn	Leu	Tyr	Leu	Gly	Ser	Met
65					70					75					80
Ala	Val	Ser	Asp	Leu	Leu	Ile	Leu	Leu	Gly	Leu	Pro	Phe	Asp	Leu	Tyr
				85					90					95	
Arg	Leu	Trp	Arg	Ser	Arg	Pro	Trp	Val	Phe	Gly	Pro	Leu	Leu	Cys	Arg
			100					105					110		
Leu	Ser	Leu	Tyr	Val	Gly	Glu	Gly	Cys	Thr	Tyr	Ala	Thr	Leu	Leu	His
		115					120					125			
Met	Thr	Ala	Leu	Ser	Val	Glu	Arg	Tyr	Leu	Ala	Ile	Cys	Arg	Pro	Leu
	130					135					140				
Arg	Ala	Arg	Val	Leu	Val	Thr	Arg	Arg	Arg	Val	Arg	Ala	Leu	Ile	Ala
145				150						155					160
Val	Leu	Trp	Ala	Val	Ala	Leu	Leu	Ser	Ala	Gly	Pro	Phe	Leu	Phe	Leu
				165					170					175	
Val	Gly	Val	Glu	Gln	Asp	Pro	Gly	Ile	Ser	Val	Val	Pro	Gly	Leu	Asn
			180					185					190		
Gly	Thr	Ala	Arg	Ile	Ala	Ser	Ser	Pro	Leu	Ala	Ser	Ser	Pro	Pro	Leu
		195					200					205			
Trp	Leu	Ser	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Pro	Ser	Gly	Pro	Glu	Thr
	210					215					220				
Ala	Glu	Ala	Ala	Ala	Leu	Phe	Ser	Arg	Glu	Cys	Arg	Pro	Ser	Pro	Ala
225					230					235					240
Gln	Leu	Gly	Ala	Leu	Arg	Val	Met	Leu	Trp	Val	Thr	Thr	Ala	Tyr	Phe
				245					250					255	
Phe	Leu	Pro	Phe	Leu	Cys	Leu	Ser	Ile	Leu	Tyr	Gly	Leu	Ile	Gly	Arg
			260					265					270		
Glu	Leu	Trp	Ser	Ser	Arg	Arg	Pro	Leu	Arg	Gly	Pro	Ala	Ala	Ser	Gly
		275					280					285			
Arg	Glu	Arg	Gly	His	Arg	Gln	Thr	Val	Arg	Val	Leu	Leu	Val	Val	Val
	290					295					300				

Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile
 305 310 315 320
 Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe
 325 330 335
 Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro
 340 345 350
 Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Ala Phe Lys
 355 360 365
 Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg
 370 375 380
 Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly
 385 390 395 400
 Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly
 405 410

<210> 11
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1161)

<400> 11

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 Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro
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ttt ccc ctg ggg gcg ctg gtg ccg gtg acc gct gtg tgc ctg tgc ctg 144
 Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu
 35 40 45

ttc gtc gtc ggg gtg agc ggc aac gtg gtg acc gtg atg ctg atc ggg 192
 Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly
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cgc tac cgg gac atg cgg acc acc acc aac ttg tac ctg ggc agc atg	240
Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met	
65 70 75 80	
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Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr	
85 90 95	
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Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg	
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Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His	
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atg acc gcg ctc agc gtc gag cgc tac ctg gcc atc tgc cgc ccg ctc	432
Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu	
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Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala	
145 150 155 160	
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Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu	
165 170 175	
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Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn	
180 185 190	
ggc acc gcg cgg atc gcc tcc tcg cct ctc gcc tcg tcg ccg cct ctc	624
Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu	
195 200 205	
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Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr	
210 215 220	

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ttc ctg ccc ttt ctg tgc ctc agc atc ctc tac ggg ctc atc ggg cgg Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg 260 265 270	816
gag ctg tgg agc agc cgg cgg ccg ctg cga ggc ccg gcc gcc tcg ggg Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly 275 280 285	864
cgg gag aga ggc cac cgg cag acc gtc cgc gtc ctg cgt aag tgg agc Arg Glu Arg Gly His Arg Gln Thr Val Arg Val Leu Arg Lys Trp Ser 290 295 300	912
cgc cgt ggt tcc aaa gac gcc tgc ctg cag tcc gcc ccg ccg ggg acc Arg Arg Gly Ser Lys Asp Ala Cys Leu Gln Ser Ala Pro Pro Gly Thr 305 310 315 320	960
gcg caa acg ctg ggt ccc ctt ccc ctg ctc gcc cag ctc tgg gcg ccg Ala Gln Thr Leu Gly Pro Leu Pro Leu Leu Ala Gln Leu Trp Ala Pro 325 330 335	1008
ctt cca gct ccc ttt cct att tcg att cca gcc tcc acc cgc cgt ggt Leu Pro Ala Pro Phe Pro Ile Ser Ile Pro Ala Ser Thr Arg Arg Gly 340 345 350	1056
ggt ggt tct ggc att tat aat ttg ctg gtt gcc ctt cca cgt tgg cag Gly Gly Ser Gly Ile Tyr Asn Leu Leu Val Ala Leu Pro Arg Trp Gln 355 360 365	1104
aat cat tta cat aaa cac gga aga ttc gcg gat gat gta ctt ctc tca Asn His Leu His Lys His Gly Arg Phe Ala Asp Asp Val Leu Leu Ser 370 375 380	1152

gta ctt taa
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385

1161

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Arg	Leu	Trp	Arg	Ser	Arg	Pro	Trp	Val	Phe	Gly	Pro	Leu	Leu	Cys	Arg
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Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala
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 Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe
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 Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg
 260 265 270
 Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly
 275 280 285
 Arg Glu Arg Gly His Arg Gln Thr Val Arg Val Leu Arg Lys Trp Ser
 290 295 300
 Arg Arg Gly Ser Lys Asp Ala Cys Leu Gln Ser Ala Pro Pro Gly Thr
 305 310 315 320
 Ala Gln Thr Leu Gly Pro Leu Pro Leu Leu Ala Gln Leu Trp Ala Pro
 325 330 335
 Leu Pro Ala Pro Phe Pro Ile Ser Ile Pro Ala Ser Thr Arg Arg Gly
 340 345 350
 Gly Gly Ser Gly Ile Tyr Asn Leu Leu Val Ala Leu Pro Arg Trp Gln
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